

10/559711

IAP16 Rec'd 07/07/PTO 05 DEC 2005

- 1 -

SEQUENCE LISTING

<110> The Walter and Eliza Hall Institute of Medical Research

<120> Active compounds and uses therefor

<130> 12456910/EJH

<140> AU 2003902788

<141> 2003-06-04

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 682

<212> DNA

<213> human

<220>

<221> CDS

<222> (1)..(678)

<223>

<400> 1

atg gtc acc cac agc aag ttt ccc gcc gcc ggg atg agc cgc ccc ctg	48
Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu	
1 5 10 15	

gac acc agc ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag	96
Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln	
20 25 30	

ctg gtg gtg aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg	144
Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp	
35 40 45	

agc gca gtg acc ggc ggc gag gcg aac ctg ctg ctc agc gcc gag ccc	192
Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Ser Ala Glu Pro	
50 55 60	

gcc ggc acc ttt ctg atc cgc gac agc tcg gac cag cgc cac ttc ttc	240
Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe	
65 70 75 80	

acg ctc agc gtc aag acc cag tct ggg acc aag aac ctg cgc atc cag	288
Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln	
85 90 95	

tgt gag ggg ggc agc ttc tct ctg cag agc gat ccc cgg agc acg cag	336
Cys Glu Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln	
100 105 110	

ccc gtg ccc cgc ttc gac tgc gtg ctc aag ctg gtg cac cac tac atg	384
Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met	
115 120 125	

ccg ccc cct gga gcc ccc tcc ttc ccc tcg cca cct act gaa ccc tcc Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser 130 135 140	432
tcc gag gtg ccc gag cag ccg tct gcc cag cca ctc cct ggg agt ccc Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro 145 150 155 160	480
ccc aga aga gcc tat tac atc tac tcc ggg ggc gag aag atc ccc ctg Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu 165 170 175	528
gtg ttg agc cgg ccc ctc tcc tcc aac gtg gcc act ctt cag cat ctc Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu 180 185 190	576
tgt cgg aag acc gtc aac ggc cac ctg gac tcc tat gag aaa gtc acc Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr 195 200 205	624
cag ctg ccg ggg ccc att cgg gag ttc ctg gac cag tac gat gcc ccg Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro 210 215 220	672
ctt taa gggg Leu 225	682
<210> 2	
<211> 225	
<212> PRT	
<213> human	
<400> 2	
Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu 1 5 10 15	
Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln 20 25 30	
Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp 35 40 45	
Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro 50 55 60	
Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe 65 70 75 80	
Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln 85 90 95	
Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln 100 105 110	
Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met	

115	120	125
Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser		
130	135	140
Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro		
145	150	155
Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu		
165	170	175
Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu		
180	185	190
Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr		
195	200	205
Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro		
210	215	220
Leu		
225		

<210> 3
 <211> 2187
 <212> DNA
 <213> murine

<220>
 <221> CDS
 <222> (18)..(692)
 <223>

<400> 3	
cgctggctcc gtgcgcc atg gtc acc cac agc aag ttt ccc gcc gcc ggg	50
Met Val Thr His Ser Lys Phe Pro Ala Ala Gly	
1 5 10	
atg agc cgc ccc ctg gac acc agc ctg cgc ctc aag acc ttc agc tcc	98
Met Ser Arg Pro Leu Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser	
15 20 25	
aaa agc gag tac cag ctg gtg gtg aac gcc gtg cgc aag ctg cag gag	146
Lys Ser Glu Tyr Gln Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu	
30 35 40	
agc gga ttc tac-tgg agc gcc gtg acc ggc ggc gag gcg aac ctg ctg	194
Ser Gly Phe Tyr Trp Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu	
45 50 55	
ctc agc gcc gag ccc gcg ggc acc ttt ctt atc cgc gac agc tcg gac	242
Leu Ser Ala Glu Pro Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp	
60 65 70 75	
cag cgc cac ttc ttc acg ttg agc gtc aag acc cag tcg ggg acc aag	290
Gln Arg His Phe Phe Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys	
80 85 90	

aac cta cgc atc cag tgt gag ggg ggc agc ttt tcg ctg cag agt gac Asn Leu Arg Ile Gln Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp 95 100 105	338
ccc cga agc acg cag cca gtt ccc cgc ttc gac tgt gta ctc aag ctg Pro Arg Ser Thr Gln Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu 110 115 120	386
gtg cac cac tac atg ccg cct cca ggg acc ccc tcc ttt tct ttg cca Val His His Tyr Met Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro 125 130 135	434
ccc acg gaa ccc tcg tcc gaa gtt ccg gag cag cca cct gcc cag gca Pro Thr Glu Pro Ser Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala 140 145 150 155	482
ctc ccc ggg agt acc ccc aag aga gct tac tac atc tat tct ggg ggc Leu Pro Gly Ser Thr Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly 160 165 170	530
gag aag att ccg ctg gta ctg agc cga cct ctc tcc tcc aac gtg gcc Glu Lys Ile Pro Leu Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala 175 180 185	578
acc ctc cag cat ctt tgt cgg aag act gtc aac ggc cac ctg gac tcc Thr Leu Gln His Leu Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser 190 195 200	626
tat gag aaa gtg acc cag ctg cct gga ccc att cgg gag ttc ctg gat Tyr Glu Lys Val Thr Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp 205 210 215	674
cag tat gat gct cca ctt taaggagcaa aagggtcaga ggggggcctg Gln Tyr Asp Ala Pro Leu 220 225	722
ggtcggtcgg tcgcctctcc tccgaggcac atggcacaag cacaaaaatc cagccccaac	782
ggtcggtagc tcccagtgag ccaggggcag attggcttct tcctcaggcc ctccactccc	842
gcagagtaga gctggcagga cctggaattc gtctgagggg agggggagct gccacctgct	902
ttccccctc cccagctcc agcttctttc aagtggagcc agccggcctg gcctggtggg	962
acaatacctt tgacaagcgg actctccct ccccttcctc cacacccct ctgcttccca	1022
agggaggtgg ggacacctcc aagtgttgaa cttagaactg caaggggaat cttcaaactt	1082
tcccgtgga acttgttgc gctttgattt ggtttgatca agagcaggca cctgggggaa	1142
ggatggaaga gaaaagggtg tgtgaagggt ttttatgctg gccaaagaaa taaccactcc	1202
cactgcccaa cctaggtgag gagtgggtgc tcctggctct ggggagagtg gcaaggggtg	1262
acctgaagag agctatactg gtgccaggct cctctccatg gggcagctaa tgaaacctcg	1322
cagatccctt gcaccccaaga accctccccg ttgtgaagag gcagtagcat ttagaaggga	1382

gacagatgag gctggtgagc tggccgcctt ttccaacacc gaagggaggc agatcaacag 1442
atgagccatc ttggagccca gggttccctt ggagcagatg gagggttctg ctttgtctct 1502
cctatgtggg gctaggagac tcgccttaaa tgccctctgt cccagggatg gggattggca 1562
cacaaggagc caaacacagc caataggcag agagttgagg gattcaccca ggtggctaca 1622
ggccagggga agtggctgca ggggagagac ccagtcactc caggagactc ctgagttaac 1682
actgggaaga cattggccag tcctagtcac ctctcggta gtaggtccga gagcttccag 1742
gccctgcaca gccctccttt ctcacctggg gggaggcagg aggtgatgga gaagccttcc 1802
catgccgctc acaggggcct cacgggaatg cagcagccat gcaattacct ggaactggtc 1862
ctgtgttggg gagaaacaag ttttctgaag tcaggtatgg ggctgggtgg ggcagctgtg 1922
tggtggggtg gcttttttct ctctgttttg aataatgttt acaatttgcc tcaatcactt 1982
ttataaaaat ccacctccag cccgcccctc tccccactca ggcttcgag gctgtctgaa 2042
gatgcttgaa aaactcaacc aaatcccagt tcaactcaga ctttgacat atatttatat 2102
ttatactcag aaaagaaaca ttacagtaat ttataataaa agagcactat tttttaatga 2162
aaaaaaaaa aaaaaaaaaa aaaaa 2187

<210> 4
<211> 225
<212> PRT
<213> murine

<400> 4

Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu
1 5 10 15
Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln
20 25 30
Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
35 40 45
Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro
50 55 60
Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
65 70 75 80
Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
85 90 95
Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
100 105 110
Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
115 120 125

Leu
225